

Scientific Discourse: Discourse, Data & Experiment

Nov 1, 2010

Summary

- Objectives: Integrate discourse with experiment meta-data, data and computation
- Approach: Build an application ontology to integrate
 - ▶ Discourse (SWAN, SIOC)
 - ▶ Experiment (OBI, MO, EFO etc.)
 - ▶ Computation (MyExperiment)
 - ▶ Annotation (AO)



SWAN-myExperiment-OBI V5 S Das, T Clark 1-11-10

Study

- Design (OBI: study design, planning)
- Data Acquisition (OBI: acquisition)
- Data Processing (OBI: data transformation)
- Data Analysis
- Data Interpretation (OBI: interpreting data)

Study Design

- Design (subclasses)
 - ▶ Observational
 - Case-Control
 - Cohort Study
 - Cross-sectional study
 - ▶ Interventional
- Factors
- Protocol

Data Acquisition

- Measurement
- Recording
- Assay
 - ▶ Measurement type (gene expression)
 - ▶ Technology type (microarrays)
 - Affymetrix U133AB
- Biomaterial *participates_in* Assay
- Biomaterial *has_quality* Biomaterial Characteristics
(OBI:Dependent_continuant)
- Assay *has_output* Primary Data

Data Processing, Analysis & Interpretation

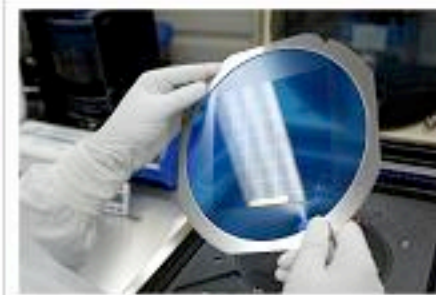
- Data Processing
 - ▶ *has_input* Primary Data
 - ▶ *has_output* Derived Data
- Data Analysis
 - ▶ *has_input* Derived Data, Design
 - ▶ *has_output* Derived Data, Claims
- Data Interpretation *has_output* Claims

Use Cases

- Produce Linked Data for interoperability of experiment repositories
 - ▶ SCF repositories (Drupal)
 - ▶ ISA-tab repositories
- Links claims in publications to experiment, data, & computation using the Annotation Ontology (AO)

Search Analysis

About Us



PD Express contains nine genome-wide expression studies and 185 human laser captured dopamine neuron and substantia nigra transcriptomes, followed by two-stage replication in 216 samples on three platforms and in incipient disease.

Top Genes

1. SNCA
2. MAPT/STH
3. NUCKS1
4. PM20D1
5. SLC41A1
6. BST1
7. LRRK2
8. USP24
9. SLC6A3
10. GBA

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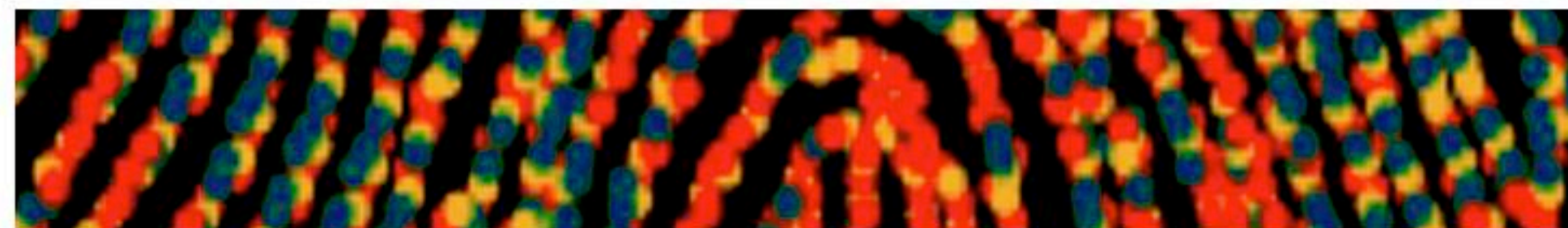


Gene Symbol

Fold Change is greater than

P-Value is less than

Search



PD Express contains nine genome-wide expression studies and 185 human laser captured dopamine neuron and substantia nigra transcriptomes, followed by two-stage replication in 216 samples on three platforms and in incipient disease.

How to Cite Content on PDExpress:

Pathway analysis of Parkinson's reveals therapeutic target for early intervention

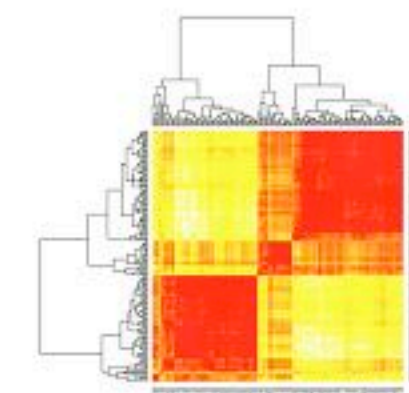
ONE-SENTENCE SUMMARY: This first world- and genome-wide pathway meta-analysis and two-stage validation reveals a pervasive expression defect of PGC-1 α -controlled bioenergetics genes in laser-captured dopamine neurons of Parkinson's patients that precedes clinical symptom onset, potentially modifies α -synuclein-induced loss of dopamine neurons, and may enable critically needed therapeutics for early intervention.

Bin Zheng¹, Zhixiang Liao¹, Joseph J. Locascio², Aron C. Eklund^{1,3}, Yanli Zhang-James⁴, Peter D. Kim⁵, Kristen A. Lesniak⁶, Marla L. Watts⁶, Michael A. Hauser⁷, Edna Grünblatt⁸, Linda B. Moran⁹, Silvia A. Mandel¹⁰, Peter Riederer⁸, Renee M. Miller¹¹, Howard J. Federoff¹², Ullrich Wüllner¹³, Spyridon Papapetropoulos¹⁴, Moussa B. Youdim¹⁰, Ippolita Cantuti-Castelvetri², Anne B. Young², Jeffery M. Vance¹⁵, Richard L. Davis¹⁶, John C. Hedreen¹⁷, Charles H. Adler¹⁸, Thomas G. Beach¹⁹, Manuel B. Graeber²⁰, Frank A. Middleton¹⁶, Jean-Christophe Rochet⁶, and Clemens R. Scherzer^{1*} for the Global PD Gene Expression (GPEx) Consortium

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Experiment Details

Researcher:

Michael A. Hauser

Type of Experiment

Affymetrix

Overall Design

Category:

Case Control

Description

Case Control study with Substantia nigra samples from 6 PD patients & 5 controls

Downloads

Data Matrix

Download All CEL Files

Analysis

Case

Control

Result

Action

PD

Control

Download Result

None

Groups

Group

Highlights

PD

Diagnosis (Parkinson's disease)

Bioassay

Subject

Diagnosis

RNA source

Data file

Age


Sex

154

PD_154

Parkinson's disease

Substantia Nigra

 [HS154..CEL](#)

74


male

185

PD_185

Parkinson's disease

Substantia Nigra

 [HS185.CEL](#)

83


male

214

PD_214

Parkinson's disease

Substantia Nigra

 [HS214.CEL](#)

83.6


male

258

PD_258

Parkinson's disease

Substantia Nigra

 [HS258.CEL](#)

79


female

81A

PD_81

Parkinson's disease

Substantia Nigra

 [HS81A.CEL](#)

87


male

872

PD_872

Parkinson's disease

Substantia Nigra

 [HS872.CEL](#)

82.4

female

Control

Diagnosis (Control without neurodegenerative disease)

Bioassay

Subject

Diagnosis

RNA source

Data file

Age


Sex

1035

control_1035

Control without neurodegenerative disease

Substantia Nigra

 [HS1035.CEL](#)

72.4


female

1037

control_1037

Control without neurodegenerative disease

Substantia Nigra

 [HS1037.CEL](#)

88


female

543B

control_543

Control without neurodegenerative disease

Substantia Nigra

 [HS543B.CEL](#)

72


female

673

control_673

Control without neurodegenerative disease

Substantia Nigra

 [HS673.CEL](#)

80.7


female

911

control_911

Control without neurodegenerative disease

Substantia Nigra

 [HS911.CEL](#)

90

male



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measurement

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technology

Filter on technology

platform

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views

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searchindex

COMPOUND-CENTRIC [VIEW](#)

browsestudies

38 public studies containing 772 assays

Investigation	Study				Assay		
	Acc	Acc	Title	Organism	Factor	Measurement	Technology
SYSCO-I-1		SYSCO-S-3	human immune response in multiple immune related cells/treatments	Homo sapiens (Human)	cell type	transcription profiling	nucleotide sequencing
SYSCO-I-1		SYSCO-S-2	Bioinformatics studies of human macrophage response to Leishmania infection	Homo sapiens (Human)	time, infection status, donor	transcription profiling	DNA microarray
						protein expression profiling	gel electrophoresis
SYSCO-I-1		SYSCO-S-1	Bioinformatics studies of mouse macrophage response to Leishmania infection for Balbc and C57Bl6 mouse strains	Mus musculus (Mouse)	Time, Infection status, Strain	transcription profiling	DNA microarray
		DEPINHO-S-2	PLAGL2 regulates Wnt signaling to impede differentiation in neural stem cells and glioma	Mus musculus (Mouse)	genetic modification	transcription profiling	DNA microarray
		DEPINHO-S-1	p53 and Pten control neural and glioma stem/progenitor cell renewal and differentiation	Mus musculus (Mouse)	genetic modification, cell type	transcription profiling	DNA microarray
		SB-S-8	StemBase E22: Gene Expression Analysis of Neural Stem Cells	Mus musculus (Mouse)	cell growth conditions, cell type	transcription profiling	DNA microarray
		SB-S-9	StemBase 26: 3T3 Fibroblasts	Mus musculus (Mouse)	culture conditions	transcription profiling	DNA microarray
		SB-S-11	StemBase E30: Temporal Analysis of Differentiating Limb Bud Mesenchymal Cell Gene Expression	Mus musculus (Mouse)	days in culture	transcription profiling	DNA microarray
		SB-S-12	StemBase E37: Role of Smad7 in Hematopoietic (M-O7e) and Non-Hematopoietic (PG13) Stem Cells	Homo sapiens (Human), Mus musculus (Mouse)	genetic modification, cell line	transcription profiling	DNA microarray
			StemBase 43: Molecular Signatures Orchestrating the Fate of Human	Homo sapiens	CD38	transcription	

Sample ISA-TAB

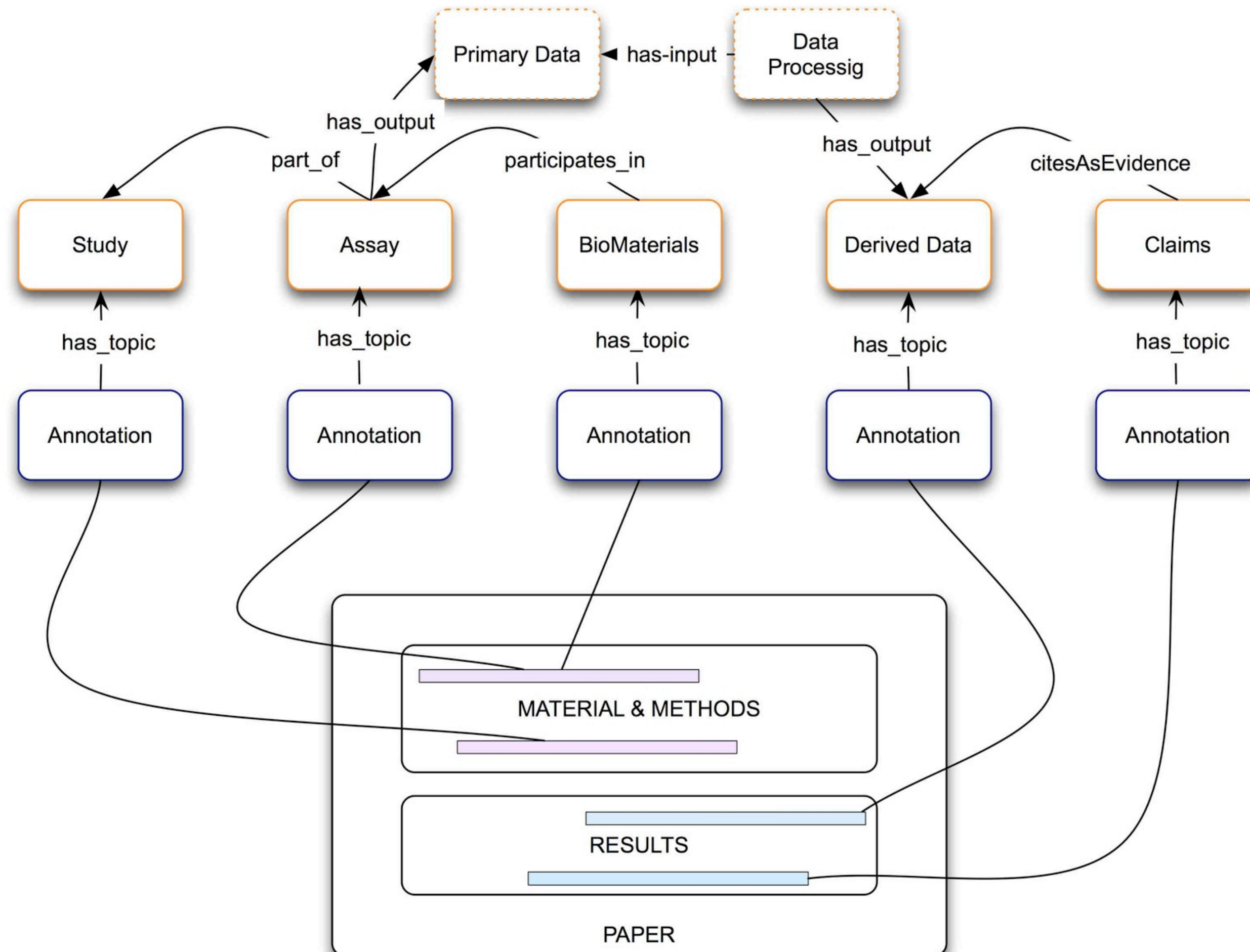
Source Name	patient unique identifier
Characteristics[organism]	Homo sapiens
Characteristics[body weight]	reduced body weight
Characteristics[disease]	osteosarcoma
Protocol REF	sample collection
Sample Name	sample unique identifier
Characteristics[organism part]	veinous blood
Characteristics[collected volume]	5 ml

'patient unique identifier' *identifies* instance(Homo sapiens [TaxID:9606])
'patient' is_a instance(Homo sapiens [TaxID:9606])

instance (Homo sapiens [TaxID:9606]) *has_quality* (decreased body weight [HP:0004325])
instance (Homo sapiens [TaxID:9606]) *has_quality* (disease [HP:0004325])
instance (Homo sapiens [TaxID:9606]) *has_quality* (decreased body weight [HP:0004325])
instance (Homo sapiens [TaxID:9606]) is_input_of process (sample_collection)

instance (portion of veinous blood [TaxID:9606]) *is_output_of* process (sample_collection)
instance (portion of veinous blood [TaxID:9606]) *has_quality* (volume of 5 ml)

Linking Claims with Data + Experiment



Next Steps

- Publish v 0.2 Ontology
 - ▶ <http://purl.org/swan/2.0/experiments/>
- Produce RDF-XML of study from SCF & ISA-tab repositories

Contributors

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